SEQUENCE PROTOCOL

<110> Degussa AG

<120> Process for the fermentative preparation of
L-amino acids using strains of the
Enterobacteriaceae family.

<130> 000425 BT

<140>
<141>

<160> 19

<170> PatentIn Ver. 2.1

<210> 1
<211> 1622
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1620)
<223> pckA

<400> 1

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 1               5                  10                  15

atc agt gac gta cat gat atc gtt tac aac cca agc tac gac ctg ctg    96
Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
            20                  25                  30

tat cag gaa gag ctc gat ccg agc ctg aca ggt tat gag cgc ggg gtg   144
Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
        35                  40                  45

tta act aat ctg ggt gcc gtt gcc gtc gat acc ggg atc ttc acc ggt   192
Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
    50                  55                  60

cgt tca cca aaa gat aag tat atc gtc cgt gac gat acc act cgc gat   240
Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
 65                  70                  75                  80

act ttc tgg tgg gca gac aaa ggc aaa ggt aag aac gac aac aaa cct   288
Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
                85                  90                  95

ctc tct ccg gaa acc tgg cag cat ctg aaa ggc ctg gtg acc agg cag   336
Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
            100                 105                 110

ctt tcc ggc aaa cgt ctg ttc gtt gtc gac gct ttc tgt ggt gcg aac   384
Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
            115                 120                 125
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      ccg gat act cgt ctt tcc gtc cgt ttc atc acc gaa gtg gcc tgg cag   432
      Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
          130             135             140

  5   gcg cat ttt gtc aaa aac atg ttt att cgc ccg agc gat gaa gaa ctg   480
      Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
      145             150             155             160

 10   gca ggt ttc aaa cca gac ttt atc gtt atg aac ggc gcg aag tgc act   528
      Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
                  165             170             175

      aac ccg cag tgg aaa gaa cag ggt ctc aac tcc gaa aac ttc gtg gcg   576
      Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
 15               180             185             190

      ttt aac ctg acc gag cgc atg cag ctg att ggc ggc acc tgg tac ggc   624
      Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
                  195             200             205
 20
      ggc gaa atg aag aaa ggg atg ttc tcg atg atg aac tac ctg ctg ccg   672
      Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
          210             215             220

 25   ctg aaa ggt atc gct tct atg cac tgc tcc gcc aac gtt ggt gag aaa   720
      Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
      225             230             235             240

      ggc gat gtt gcg gtg ttc ttc ggc ctt tcc ggc acc ggt aaa acc acc   768
      Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
 30                   245             250             255

      ctt tcc acc gac ccg aaa cgt cgc ctg att ggc gat gac gaa cac ggc   816
      Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
 35               260             265             270

      tgg gac gat gac ggc gtg ttt aac ttc gaa ggc ggc tgc tac gca aaa   864
      Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
                  275             280             285
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      act atc aag ctg tcg aaa gaa gcg gaa cct gaa atc tac aac gct atc   912
      Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
          290             295             300

 45   cgt cgt gat gcg ttg ctg gaa aac gtc acc gtg cgt gaa gat ggc act   960
      Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
      305             310             315             320

      atc gac ttt gat gat ggt tca aaa acc gag aac acc cgc gtt tct tat  1008
 50   Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
                  325             330             335

      ccg atc tat cac atc gat aac att gtt aag ccg gtt tcc aaa gcg ggc  1056
      Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
 55               340             345             350

      cac gcg act aag gtt atc ttc ctg act gct gat gct ttc ggc gtg ttg  1104
      His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
          355             360             365
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ccg ccg gtt tct cgc ctg act gcc gat caa acc cag tat cac ttc ctc      1152
Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
    370             375             380

tct ggc ttc acc gcc aaa ctg gcc ggt act gag cgt ggc atc acc gaa      1200
Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
385             390             395             400

ccg acg cca acc ttc tcc gct tgc ttc ggc gcg gca ttc ctg tcg ctg      1248
Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
            405             410             415

cac ccg act cag tac gca gaa gtg ctg gtg aaa cgt atg cag gcg gcg      1296
His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
        420             425             430

ggc gcg cag gct tat ctg gtt aac act ggc tgg aac ggc act ggc aaa      1344
Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
        435             440             445

cgt atc tcg att aaa gat acc cgc gcc att atc gac gcc atc ctc aac      1392
Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
    450             455             460

ggt tcg ctg gat aat gca gaa acc ttc act ctg ccg atg ttt aac ctg      1440
Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
465             470             475             480

gcg atc cca acc gaa ctg ccg ggc gta gac acg aag att ctc gat ccg      1488
Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
            485             490             495

cgt aac acc tac gct tct ccg gaa cag tgg cag gaa aaa gcc gaa acc      1536
Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
            500             505             510

ctg gcg aaa ctg ttt atc gac aac ttc gat aaa tac acc gac acc cct      1584
Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
    515             520             525

gcg ggt gcc gcg ctg gta gcg gct ggt ccg aaa ctg taa                  1623
Ala Gly Ala Ala Leu Val Ala Ala Gly Pro Lys Leu
530             535             540
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<211> 540
<212> PRT
<213> Escherichia coli

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Ile Ser Asp Val His Asp Ile Val Tyr Asn Pro Ser Tyr Asp Leu Leu
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Tyr Gln Glu Glu Leu Asp Pro Ser Leu Thr Gly Tyr Glu Arg Gly Val
        35              40              45
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4

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          Leu Thr Asn Leu Gly Ala Val Ala Val Asp Thr Gly Ile Phe Thr Gly
              50              55              60
      5   Arg Ser Pro Lys Asp Lys Tyr Ile Val Arg Asp Asp Thr Thr Arg Asp
              65              70              75              80
          Thr Phe Trp Trp Ala Asp Lys Gly Lys Gly Lys Asn Asp Asn Lys Pro
                      85              90              95
     10   Leu Ser Pro Glu Thr Trp Gln His Leu Lys Gly Leu Val Thr Arg Gln
                  100             105             110
          Leu Ser Gly Lys Arg Leu Phe Val Val Asp Ala Phe Cys Gly Ala Asn
                  115             120             125
     15   Pro Asp Thr Arg Leu Ser Val Arg Phe Ile Thr Glu Val Ala Trp Gln
                  130             135             140
     20   Ala His Phe Val Lys Asn Met Phe Ile Arg Pro Ser Asp Glu Glu Leu
              145             150             155             160
          Ala Gly Phe Lys Pro Asp Phe Ile Val Met Asn Gly Ala Lys Cys Thr
                      165             170             175
     25   Asn Pro Gln Trp Lys Glu Gln Gly Leu Asn Ser Glu Asn Phe Val Ala
                      180             185             190
          Phe Asn Leu Thr Glu Arg Met Gln Leu Ile Gly Gly Thr Trp Tyr Gly
                  195             200             205
     30   Gly Glu Met Lys Lys Gly Met Phe Ser Met Met Asn Tyr Leu Leu Pro
              210             215             220
     35   Leu Lys Gly Ile Ala Ser Met His Cys Ser Ala Asn Val Gly Glu Lys
          225             230             235             240
          Gly Asp Val Ala Val Phe Phe Gly Leu Ser Gly Thr Gly Lys Thr Thr
                      245             250             255
     40   Leu Ser Thr Asp Pro Lys Arg Arg Leu Ile Gly Asp Asp Glu His Gly
                  260             265             270
          Trp Asp Asp Asp Gly Val Phe Asn Phe Glu Gly Gly Cys Tyr Ala Lys
                  275             280             285
     45   Thr Ile Lys Leu Ser Lys Glu Ala Glu Pro Glu Ile Tyr Asn Ala Ile
                  290             295             300
     50   Arg Arg Asp Ala Leu Leu Glu Asn Val Thr Val Arg Glu Asp Gly Thr
          305             310             315             320
          Ile Asp Phe Asp Asp Gly Ser Lys Thr Glu Asn Thr Arg Val Ser Tyr
                      325             330             335
     55   Pro Ile Tyr His Ile Asp Asn Ile Val Lys Pro Val Ser Lys Ala Gly
                  340             345             350
          His Ala Thr Lys Val Ile Phe Leu Thr Ala Asp Ala Phe Gly Val Leu
     60       355             360             365
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        Pro Pro Val Ser Arg Leu Thr Ala Asp Gln Thr Gln Tyr His Phe Leu
            370             375             380

  5     Ser Gly Phe Thr Ala Lys Leu Ala Gly Thr Glu Arg Gly Ile Thr Glu
        385             390             395             400

        Pro Thr Pro Thr Phe Ser Ala Cys Phe Gly Ala Ala Phe Leu Ser Leu
                    405             410             415

 10     His Pro Thr Gln Tyr Ala Glu Val Leu Val Lys Arg Met Gln Ala Ala
                    420             425             430

        Gly Ala Gln Ala Tyr Leu Val Asn Thr Gly Trp Asn Gly Thr Gly Lys
            435             440             445
 15
        Arg Ile Ser Ile Lys Asp Thr Arg Ala Ile Ile Asp Ala Ile Leu Asn
            450             455             460

 20     Gly Ser Leu Asp Asn Ala Glu Thr Phe Thr Leu Pro Met Phe Asn Leu
        465             470             475             480

        Ala Ile Pro Thr Glu Leu Pro Gly Val Asp Thr Lys Ile Leu Asp Pro
                    485             490             495

 25     Arg Asn Thr Tyr Ala Ser Pro Glu Gln Trp Gln Glu Lys Ala Glu Thr
                500             505             510

        Leu Ala Lys Leu Phe Ile Asp Asn Phe Asp Lys Tyr Thr Asp Thr Pro
            515             520             525
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        Ala Gly Ala Ala Leu Val Ala Ala Gly Pro Lys Leu
        530             535             540


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        <211> 1156
        <212> DNA
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        <220>
        <221> misc_feature
        <222> (1)..(1156)
        <223> Mutagene DNA
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        <221> misc_feature
        <222> (1)..(35)
        <223> Technical DNA/residues of the polylinker sequence
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        <220>
        <221> misc_feature
        <222> (36)..(522)
        <223> Part of the 5' region (pck1) of the pckA gene
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        <220>
        <221> misc_feature
        <222> (523)..(542)
        <223> Technical DNA/residues of the polylinker sequence
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        <220>
        <221> misc_feature
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<222> (543)..(1105)
<223> Part of the 3' region (pck2) of the pckA gene

<220>
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<222> (1106)..(1156)
<223> Technical DNA/residues of the polylinker sequence

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caccaaaaga taagtatatc gtccgtgacg ataccactcg cgatactttc tggtgggcag 180
acaaaggcaa aggtaagaac gacaacaaac ctctctctcc ggaaacctgg cagcatctga 240
aaggcctggt gaccaggcag ctttccggca aacgtctgtt cgttgtcgac gctttctgtg 300
gtgcgaaccc ggatactcgt ctttccgtcc gtttcatcac cgaagtggcc tggcaggcgc 360
attttgtcaa aaacatgttt attcgcccga gcgatgaaga actggcaggt ttcaaaccag 420
actttatcgt tatgaacggc gcgaagtgca ctaacccgca gtggaaagaa cagggtctca 480
actccgaaaa cttcgtggcg tttaacctga ccgagcgcat gcaagccgaa ttctgcagat 540
cctgaagatg gcactatcga ctttgatgat ggttcaaaaa ccgagaacac ccgcgtttct 600
tatccgatct atcacatcga taacattgtt aagccggttt ccaaagcggg ccacgcgact 660
aaggttatct tcctgactgc tgatgctttc ggcgtgttgc cgccggtttc tcgcctgact 720
gccgatcaaa cccagtatca cttcctctct ggcttcaccg ccaaactggc cggtactgag 780
cgtggcatca ccgaaccgac gccaaccttc tccgcttgct tcggcgcggc attcctgtcg 840
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gcttatctgg ttaacactgg ctggaacggc actggcaaac gtatctcgat taaagatacc 960
cgcgccatta tcgacgccat cctcaacggt tcgctggata atgcagaaac cttcactctg 1020
ccgatgttta acctggcgat cccaaccgaa ctgccgggcg tagacacgaa gattctcgat 1080
ccgcgtaaca cctacgcttc tccggaagcc gaattctgca gatatccatc acactggcgg 1140
ccgctcgagc atgcat                                                  1156


<210> 4
<211> 1294
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)..(3)
<223> Start codon of the delta pckA allele

<220>
<221> misc_feature
<222> (1)..(598)
<223> 5' region of the delta pckA allele

<220>
<221> misc_feature
<222> (599)..(618)
<223> Technical DNA/residues of the polylinker sequence

<220>
<221> misc_feature
<222> (619)..(1291)
<223> 3' region of the delta pckA allele

<220>
<221> misc_feature
<222> (1292)..(1294)
<223> Stop codon of the delta pckA allele

<400> 4
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            atgcgcgtta acaatggttt gaccccgcaa gaactcgagg cttatggtat cagtgacgta   60
            catgatatcg tttacaaccc aagctacgac ctgctgtatc aggaagagct cgatccgagc  120
            ctgacaggtt atgagcgcgg ggtgttaact aatctgggtg ccgttgccgt cgataccggg  180
            atcttcaccg gtcgttcacc aaaagataag tatatcgtcc gtgacgatac cactcgcgat  240
      5     actttctggt gggcagacaa aggcaaaggt aagaacgaca acaaacctct ctctccggaa  300
            acctggcagc atctgaaagg cctggtgacc aggcagcttt ccggcaaacg tctgttcgtt  360
            gtcgacgctt tctgtggtgc gaacccggat actcgtcttt ccgtccgttt catcaccgaa  420
            gtggcctggc aggcgcattt tgtcaaaaac atgtttattc gcccgagcga tgaagaactg  480
            gcaggtttca aaccagactt tatcgttatg aacggcgcga agtgcactaa cccgcagtgg  540
     10     aaagaacagg gtctcaactc cgaaaacttc gtggcgttta acctgaccga gcgcatgcaa  600
            gccgaattct gcagatcctg aagatggcac tatcgacttt gatgatggtt caaaaaccga  660
            gaacacccgc gtttcttatc cgatctatca catcgataac attgttaagc cggtttccaa  720
            agcgggccac gcgactaagg ttatcttcct gactgctgat gctttcggcg tgttgccgcc  780
            ggtttctcgc ctgactgccg atcaaaccca gtatcacttc ctctctggct tcaccgccaa  840
     15     actggccggt actgagcgtg gcatcaccga accgacgcca accttctccg cttgcttcgg  900
            cgcggcattc ctgtcgctgc acccgactca gtacgcagaa gtgctggtga aacgtatgca  960
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            ctcgattaaa gatacccgcg ccattatcga cgccatcctc aacggttcgc tggataatgc 1080
            agaaaccttc actctgccga tgtttaacct ggcgatccca accgaactgc cgggcgtaga 1140
     20     cacgaagatt ctcgatccgc gtaacaccta cgcttctccg gaacagtggc aggaaaaagc 1200
            cgaaaccctg gcgaaactgt ttatcgacaa cttcgataaa tacaccgaca cccctgcggg 1260
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            <223> ORF ytfP

     35   <220>
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            <222> Complement((461)..(727))
            <223> ORF yjfA

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            ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacaccca  180
            gggagtaggc gactcctccc aggtagtggt cagcggctat gtattgccag gtctgcaagt  240
     45     gaaatacggc gtgggtatat ttgactctat agcaacactc acgttacgtt atcgcctgat  300
            gcctaagcta tatctggaag ccgtgtctgg tgtagaccag gcactggatt tgctctatca  360
            gttcgagttt tagcaatgcg aatatttgtc tacggcagtt tacgccacaa acaaggcaac  420
            agtcactgga tgaccaatgc ccagttactg ggcgatttca gtatcgataa ctaccagttg  480
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     50     tatcgtattg acaacgccac gctggccgaa cttgatgcct tgcgcaccag gggcggtgaa  600
            tacgcgcgcc agttgattca gacgccgtac gggagtgcat ggatgtacgt ttatcaacga  660
            cccgtcgatg gattaaagct aattgaaagc ggcgactggt tagacaggga taagtaacca  720
            tatgcatacg ccacctttcg gtggcgttgt tttttgcgag acgactcgca ttctgttttg  780
            taattccctc acctttttct tttctctccg agccgctttc catatctatt aacgcataaa  840
     55     aaactctgct ggcattcaca aatcgcgcagg ggtaaaacgt ttcctgtagc accgtgagtt  900
            atactttgta taacttaagg aggtgcagat gcgtattacc ataaaaagat gggggaacag  960
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            gcttgatgaa ctgctggcac agtgtgacat gaacgccgcg gaacttagcg agcaggatgt 1140
     60     ctggggtaaa tccacccctg cgggtgacga atatggtaa agaaaagtga atttgaacgg 1200
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<210> 6
<211> 911
<212> DNA
<213> Escherichia coli

<220>
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<222> (1)..(911)
<223> Deletion-carrying ytfP-yjfA region

<220>
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<222> (1)..(383)
<223> 5' flank of the ytfP-yjfA region

<220>
<221> misc_feature
<222> (384)..(911)
<223> 3' flank of the ytfP-yjfA region

<220>
<221> misc_feature
<222> (376)..(378)
<223> ATG codon of the truncated ORF ytfP

<220>
<221> misc_feature
<222> Complement((388)..(390))
<223> ATG codon of the truncated ORF yjfA

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ggcgatgtcg caacaagctg ccttgtctta tttgctacgt ggacaagggc tggagagcga 60
tcagagcgac agtgcggcaa tgacctcgat gctgattggt ttggggggttg cgcaaagtgg 120
ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacaccca 180
gggagtaggc gactcctccc aggtagtggt cagcggctat gtattgccag gtctgcaagt 240
gaaatacggc gtgggtatat ttgactctat agcaacactc acgttacgtt atcgcctgat 300
gcctaagcta tatctggaag ccgtgtctgg tgtagaccag gcactggatt tgctctatca 360
gttcgagttt tagcaatgcg aattatgcat acgccacctt cgggtggcgt tgtttttgc 420
gagacgactc gcattctgtt ttgtaattcc ctcacctttt gcttttctct ccgagccgct 480
ttccatatct attaacgcat aaaaaactct gctggcattc acaaatgcgc aggggtaaaa 540
cgtttcctgt agcaccgtga gttatactttt gtataactta aggaggtgca gatgcgtatt 600
accataaaaa gatgggggaa cagtgcaggt atggtcattc ccaatatcgt aatgaaagaa 660
cttaacttac agccggggca gagcgtggag cgcaagtga gcaacaatca actgattctg 720
acacccatct ccaggcgcta ctcgcttgat gaactgctgg cacagtgtga catgaacgcc 780
gcggaactta gcgagcagga tgtctggggt aaatccaccc ctgcgggtga cgaaatatgg 840
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gccatgaaca g                                                    911


<210> 7
<211> 1158
<212> DNA
<213> Escherichia coli

<220>
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<222> (1)..(1158)
<223> Deletion-carrying ytfP-yjfA region

<220>
<221> misc_feature
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<222> (1)..(630)
<223> 5' flank of the ytfP-yjfA region

<220>
<221> misc_feature
<222> (631)..(1158)
<223> 3' flank of the ytfP-yjfA region

<220>
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<223> ATG codon of the truncated ORF ytfP

<220>
<221> misc_feature
<222> Complement((635)..(637))
<223> ATG codon of the truncated ORF yjfA

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ccagattgtg ggtaaaatcg gcgagacgtt tggcgtaagc aatttagcgc tcgacaccca 180
gggagtaggc gactcctccc aggtagtggt cagcggctat gtattgccag gtctgcaagt 240
gaaatacggc gtgggtatat ttgactctat agcaacactc acgttacgtt atcgcctgat 300
gcctaagcta tatctggaag ccgtgtctgg tgtagaccag gcactggatt tgctctatca 360
gttcgagttt tagcaatgcg aatatttgtc tacggcagtt tacgccacaa acaaggcaac 420
agtcactgga tgaccaatgc ccagttactg ggcgatttca gtatcgataa ctaccagttg 480
tatagcctgg gccactatcc aggcgcagtt ccggggaacg gaacggtaca cggtgaagtt 540
tatcgtattg acaacgccac gctggccgaa cttgatgcct tgcgcaccag gggcggtgaa 600
tacgcgcgcc agttgattca gacgccgtac tatgcatacg ccaccttcgg gtggcgttgt 660
ttttttgcgag acgactcgca ttctgtttttg taattccctc accttttgct tttctctccg 720
agccgctttc catatctatt aacgcataaa aaactctgct ggcattcaca aatgcgcagg 780
ggtaaaacgt ttcctgtagc accgtgagtt atactttgta taacttaagg aggtgcagat 840
gcgtattacc ataaaaagat gggggaacag tgcaggtatg gtcattccca atatcgtaat 900
gaaagaactt aacttacagc cggggcagag cgtggaggcg caagtgagca acaatcaact 960
gattctgaca cccatctcca ggcgctactc gcttgatgaa ctgctggcac agtgtgacat 1020
gaacgccgcg gaacttagcg agcaggatgt ctggggtaaa tccacccctg cgggtgacga 1080
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gcaagcggcc atgaacag                                              1158
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<210> 8
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      pckA'5'-1

<400> 8
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gatccgagcc tgacaggtta                                             20
```

<210> 9
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      pckA'5'-2

```
<400> 9
gcatgcgctc ggtcaggtta                                                    20


<210> 10
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      pckA'3'-1

<400> 10
aggcctgaag atggcactat cg                                                 22


<210> 11
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      pckA'3'-2

<400> 11
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<210> 12
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer Gdh1

<400> 12
tgaacacttc tggcggtacg                                                    20


<210> 13
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer Gdh2

<400> 13
cctcggcgaa gctaatatgg                                                    20


<210> 14
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer RhtC1
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<400> 14
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<210> 15
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<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer RhtC2

<400> 15
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<210> 16
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence:   Primer Tdh1

<400> 16
tcgcgaccta taagtttggg                                                    20


<210> 17
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer Tdh2

<400> 17
aataccagcc cttgttcgtg                                                    20


<210> 18
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      ytfP-1

<400> 18
ggcgatgtcg caacaagctg                                                    20


<210> 19
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer
      ytfP-2
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<400> 19
ctgttcatgg ccgcttgctg   20